Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE.

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Public Summary:

Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. Qiu P, Simonds EF, Bendall SC, Gibbs KD, Bruggner RV, Linderman MD, Sachs K, Nolan GP, Plevritis SK. (2011) Nat Biotechnol. 2011;29(10) The ability to analyze multiple single-cell parameters is critical for understanding cellular heterogeneity. Despite recent advances in measurement technology, methods for analyzing high-dimensional single-cell data are often subjective, labor intensive and require prior knowledge of the biological system. To objectively uncover cellular heterogeneity from single-cell measurements, we present a versatile computational approach, spanning-tree progression analysis of density-normalized events (SPADE). We applied SPADE to flow cytometry data of mouse bone marrow and to mass cytometry data of human bone marrow. In both cases, SPADE organized cells in a hierarchy of related phenotypes that partially recapitulated well-described patterns of hematopoiesis. We demonstrate that SPADE is robust to measurement noise and to the choice of cellular markers. SPADE facilitates the analysis of cellular heterogeneity, the identification of cell types and comparison of functional markers in response to perturbations.

Scientific Abstract:

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